

**Data S1.** The obtained sequence coverage of human TRPA1 and  $\Delta 1$ -688 human TRPA1 by mass spectrometry in trypsin or chymotrypsin digestions. The red colored residues were detected in peptides resulting from the digestion with the specified enzyme, whereas black colored residues were not detected.

**hTRPA1 sequence coverage of 76.2% by trypsin digestion**

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1 MKRSLRKMWRPGEKKEPQGVVYEDVDDTEDFKESLKVVFEGSAYGLQNFNKQKLLKRCDDMDTFFLHYAAAEGQIELMEK ITRDSSLEVLHEMDDYGNT
101 PLHCAVEKNQIESVKFLLSRGANPNLRFNFMNMAPLHIAVQGMNNEVMKVLLEHRTIDVNLEGENGTAVI IACTTNNSEALQILLKKGAKPCKSNKWGCF
201 PIHQAAFSGSKECMEIILRFGEHGYSRQLHINFMNNGKATPLHLAVQNGDLEMICKLNDGAQIDPVEKGRCTAIHFAATQGATEIVKLMISSYSGSVD
301 IVNTTDGCHETMLHRASLFDHHELADYLI SVGADINKIDSEGRSPLILATASASWNI VNNLLSKGAQVDIKDNFGRNFLHLTVQQPYGLKNLRPEFMQM
401 QIKELVMDEDNDGCTPLHYACRQGGPGSVNNLLGFNVSIHKS KDKKSPHFAASYGRINTCQRLQDISDTRLLNEGDHLGMTPLHLAAKNGHDKVVQL
501 LLKKGALFLSDHNGWTALHHSASMGGYTQTMKVILDTNLKCTDRLEDEDGNTALHFAAREGHAKAVALLSHNADIVLNKQASFLHLALHNKRKEVLTII
601 RSKRWDECLKIFSHNSPGNKCPITEMIEYLPCEMKVLLDFCMLHSTEDKSCRDYIEYNFKYLQCPLEFTKKTPTQDVIYEPLTALNAMVQNNRIELLNH
701 PVCKEYLLMKWLAYGFRAHMMNLGSYCLGLIPMTILV VNIKPGMAFNSTGIINETS DHSEILD TTNSYLIKTCMILVFLSSIFGYCKEAGQIFQQRKNYF
801 MDISNVLEWIIYTTGII FVLPFVEIPAHLQWQC GAI AVYFYWMNFLLYLQRFENCGIFIVMLEVILKTLRSTVVVFIFLLLA FGLSFYI LLNLQDPFSS
901 PLLSIIQTFSMMLGDIN YRESFLEPYLRNELAHPVLSFAQLVSFTIFVPIVLMNLLIGLAVG DIAEVQKHASLKR IAMQVELHTSLEKKLPLWFLRKVDQ
1001 KSTIVYPNKPRSGGMLFHFICFLFCTGEIRQEIPNADKSLEMEILKQKYRLKDLTF LLEKQHELIKLI IQKMEI ISETEDDDSHCSFQDRFKKEQMEQRN
1101 SRWNTVLRRAVKAKTHHLEP

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**hTRPA1 sequence coverage of 87.8% by chymotrypsin digestion**

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1 MKRSLRKMWRPGEKKEPQGVVYEDVDDTEDFKESLKVVFEGSAYGLQNFNKQKLLKRCDDMDTFFLHYAAAEGQIELMEK ITRDSSLEVLHEMDDYGNT
101 PLHCAVEKNQIESVKFLLSRGANPNLRFNFMNMAPLHIAVQGMNNEVMKVLLEHRTIDVNLEGENGTAVI IACTTNNSEALQILLKKGAKPCKSNKWGCF
201 PIHQAAFSGSKECMEIILRFGEHGYSRQLHINFMNNGKATPLHLAVQNGDLEMICKLNDGAQIDPVEKGRCTAIHFAATQGATEIVKLMISSYSGSVD
301 IVNTTDGCHETMLHRASLFDHHELADYLI SVGADINKIDSEGRSPLILATASASWNI VNNLLSKGAQVDIKDNFGRNFLHLTVQQPYGLKNLRPEFMQM
401 QIKELVMDEDNDGCTPLHYACRQGGPGSVNNLLGFNVSIHKS KDKKSPHFAASYGRINTCQRLQDISDTRLLNEGDHLGMTPLHLAAKNGHDKVVQL
501 LLKKGALFLSDHNGWTALHHSASMGGYTQTMKVILDTNLKCTDRLEDEDGNTALHFAAREGHAKAVALLSHNADIVLNKQASFLHLALHNKRKEVLTII
601 RSKRWDECLKIFSHNSPGNKCPITEMIEYLPCEMKVLLDFCMLHSTEDKSCRDYIEYNFKYLQCPLEFTKKTPTQDVIYEPLTALNAMVQNNRIELLNH
701 PVCKEYLLMKWLAYGFRAHMMNLGSYCLGLIPMTILV VNIKPGMAFNSTGIINETS DHSEILD TTNSYLIKTCMILVFLSSIFGYCKEAGQIFQQRKNYF
801 MDISNVLEWIIYTTGII FVLPFVEIPAHLQWQC GAI AVYFYWMNFLLYLQRFENCGIFIVMLEVILKTLRSTVVVFIFLLLA FGLSFYI LLNLQDPFSS
901 PLLSIIQTFSMMLGDIN YRESFLEPYLRNELAHPVLSFAQLVSFTIFVPIVLMNLLIGLAVG DIAEVQKHASLKR IAMQVELHTSLEKKLPLWFLRKVDQ
1001 KSTIVYPNKPRSGGMLFHFICFLFCTGEIRQEIPNADKSLEMEILKQKYRLKDLTF LLEKQHELIKLI IQKMEI ISETEDDDSHCSFQDRFKKEQMEQRN
1101 SRWNTVLRRAVKAKTHHLEP

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**$\Delta 1$ -688 hTRPA1 sequence coverage of 52.9% by trypsin digestion**

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689 MVQNNRIELLNH
701 PVCKEYLLMKWLAYGFRAHMMNLGSYCLGLIPMTILV VNIKPGMAFNSTGIINETS DHSEILD TTNSYLIKTCMILVFLSSIFGYCKEAGQIFQQRKNYF
801 MDISNVLEWIIYTTGII FVLPFVEIPAHLQWQC GAI AVYFYWMNFLLYLQRFENCGIFIVMLEVILKTLRSTVVVFIFLLLA FGLSFYI LLNLQDPFSS
901 PLLSIIQTFSMMLGDIN YRESFLEPYLRNELAHPVLSFAQLVSFTIFVPIVLMNLLIGLAVG DIAEVQKHASLKR IAMQVELHTSLEKKLPLWFLRKVDQ
1001 KSTIVYPNKPRSGGMLFHFICFLFCTGEIRQEIPNADKSLEMEILKQKYRLKDLTF LLEKQHELIKLI IQKMEI ISETEDDDSHCSFQDRFKKEQMEQRN
1101 SRWNTVLRRAVKAKTHHLEP

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**$\Delta 1$ -688 hTRPA1 sequence coverage of 87.5% by chymotrypsin digestion**

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689 MVQNNRIELLNH
701 PVCKEYLLMKWLAYGFRAHMMNLGSYCLGLIPMTILV VNIKPGMAFNSTGIINETS DHSEILD TTNSYLIKTCMILVFLSSIFGYCKEAGQIFQQRKNYF
801 MDISNVLEWIIYTTGII FVLPFVEIPAHLQWQC GAI AVYFYWMNFLLYLQRFENCGIFIVMLEVILKTLRSTVVVFIFLLLA FGLSFYI LLNLQDPFSS
901 PLLSIIQTFSMMLGDIN YRESFLEPYLRNELAHPVLSFAQLVSFTIFVPIVLMNLLIGLAVG DIAEVQKHASLKR IAMQVELHTSLEKKLPLWFLRKVDQ
1001 KSTIVYPNKPRSGGMLFHFICFLFCTGEIRQEIPNADKSLEMEILKQKYRLKDLTF LLEKQHELIKLI IQKMEI ISETEDDDSHCSFQDRFKKEQMEQRN
1101 SRWNTVLRRAVKAKTHHLEP

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